Please replace Claim 24 with the following new Claim 24:

24. (Twice amended) A method of detecting a disease or a disease susceptibility trait in an organism, wherein said disease or said disease susceptibility trait is associated with a germline mutation in one of two or more subject genes, comprising:

(a) isolating a biological sample from said organism;

(b) immunologically quantitating the amount of wild-type protein in said sample, that is expressed by each of the subject genes;

(c) calculating the ratio of the amount of the wild-type protein expressed by one of said subject genes in said sample, to the amount of wild-type protein expressed by the other subject gene in said sample, or to each of the amounts of wild-type protein expressed by each of the other subject genes in said sample;

(d) determining whether the ratio or ratios calculated in step (c) reflects or reflect an abnormally low level of a wild-type protein expressed by either of the subject genes, or by any of the subject genes in said sample; and

(e) concluding that if the ratio or ratios calculated in step (c) indicates or indicate that there is an abnormally low level of a wild-type protein expressed by one of the subject genes in said sample, that that subject gene contains a germline mutation in one of its alleles, and that the subject organism is

affected by the disease or the disease susceptibility trait associated with said germline mutation;

wherein said germline mutation is selected from the group consisting of truncating-causing mutations and mutations that cause allelic loss.

Please replace Claim 25 with the following new Claim 25:

25. (Amended) The method of Claim 24 wherein step (d) comprises comparing the ratio or ratios calculated in step (c) to a comparable mean or means of ratios calculated from the amounts of wild-type proteins expressed by the subject genes in comparable biological samples from organisms of the same taxonomic classification as the subject organism, wherein said organisms of the same taxonomic classification as the subject organism are unaffected by said disease or by said disease susceptibility trait.

Please replace Claim 32 with the following new Claim 32:

32. (Twice amended) The method of Claim 24 wherein said mutation is selected from the group consisting of nonsense mutations, frameshift mutations, promoter mutations, enhancer mutations, splice site mutations, null mutations, and poly-A tail mutations.